

CCTCTCCACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGAGTTGACCAG
 AGATGCAAGGGGTGAAGGAGCGCTCCTACCGTTAGGGAACTCTGGGACAGAGCGCCCC
 GGCGCCTGATGGCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTCGGGAACCATA
 CCATGGCCCAGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGC
M A R I P K T L K F V V V I V A V L L P
 CAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTCCCCAGCAGACAGTGG
V L A Y S A T T A R Q E E V P Q Q T V A
 CCCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGAT
 P Q Q Q R H S F K G E E C P A G S H R S
 CAGAACATACTGGAGCCTGTAACCGTGACAGAGGGTGTGGATTACACCAACGCTTCCA
 E H T G A C N P C T E G V D Y T N A S N
 ACAATGAACCTTCTTGCTTCCATGTACAGTTGTAATCAGATCAAAACATAAAAGTT
 N E P S C F P C T V C K S D Q K H K S S
 CCTGCACCATGACCAGAGACACAGTGTGTCAAGTGTAAAGAAGGCACCTCCGGAATGAAA
 C T M T R D T V C Q C K E G T F R N E N
 ACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTA
 S P E M C R K C S R C P S G E V Q V S N
 ATTGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGG
 C T S W D D I Q C V E E F G A N A T V E
 AAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTG
 T P A A E E T M N T S P G T P A P A A E
 AAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCA
 E T M N T S P G T P A P A A E E T M T T
 CCAGCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCAAGCCGGGACTC
 S P G T P A P A A E E T M T T S P G T P
 CTGCCCCAGCTGCTGAAGAGACAATGACCAAGCCGGGACTCCTGCCCTTCATT
 A P A A E E T M T T S P G T P A S S H Y

FIG. 1A

09826212-040504

ACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGTTT
L S C T I V G I I V L I V L L I V F V *

GAAAGACTTCACTGTGGAAGAAATTCCCTCCTTACCTGAAAGGTTCAGGTAGGCGCTGGC
TGAGGGCGGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTGCTGTGTTCCCACAGAC
AGAAACGCCTGCCCTGCCCAAGTCCTGGTGTCCAGCCTGGCTATCTTCCCT
GTGATCGTCCATCCCCACATCCCGTGCACCCCCCAGGACCCCTGGTCTCATCAGTCCCTC
TCCTGGAGCTGGGGTCCACACATCTCCAGCCAAGTCCAAGAGGCAGGGCCAGTTCC
CCATCTTCAGGCCAGCCAGGCAGGGGGCAGTCGGCTCTCAACTGGGTGACAAGGGTGA
GGATGAGAAGTGGTCACGGGATTATTACGCCCTGGTCAGAGCAGAACACAGAGATTTC
CGTAAAAAAA

FIG. 1B

FIG. 2A

FIG. 2B

FIG. 2C

FIG. 2D

Consensus #1												
149	-	-	C	L	N	G	T	V	H	L	-	S
141	-	-	K	C	R	P	G	F	G	V	A	R
128	-	-	C	E	A	G	S	G	L	V	-	F
146	-	R	L	V	L	C	Q	P	G	T	E	A
137	-	-	-	-	-	-	-	-	-	S	T	V
87	-	-	C	N	S	G	I	-	L	V	-	R
129	S	V	-	-	C	P	A	G	M	I	V	K
123	R	-	S	C	S	P	G	F	G	V	K	Q
106	-	-	C	K	Q	G	Q	E	L	T	K	G
110	-	-	R	A	G	T	Q	P	I	-	D	S
131	T	-	R	C	G	I	G	Y	G	V	S	G
131	T	-	R	C	G	I	G	Y	G	V	S	G
131	-	-	C	P	S	G	E	V	Q	V	-	S

FIG. 2E

		Consensus #1
178	E C V S C S N C K - - - - -	- - - - - K S L E C T K L C L P - - - - -
178	I C R P H Q I C N V V A - - - - -	- - - - - I P G N A S R D A V C T S T S P T R S M A P - - - - -
163	P C L P C T V C E D T E R Q - - - - -	- - - - - I P G N A S R D A V C T S T S P T R S M A P - - - - -
186	R C Q P H T R C E I Q G L V E A A P G T S Y S D T I C K N P P E P G A M L L - - - - -	- - - - - E E I P G R W I T R S N G F R - - - - -
142	H C D P C T K C E - - - - -	- - - - - E E I P G R W I T R S N G F R - - - - -
111	Q C R D - K E C T - - - - -	- - - - - H G I - - I K E C - T - - - - -
165	N C K E P S S G T I P Q - A K P T P V S P A T S S A S T M P V R G G T R L A Q E - - - - -	- - - - - E C - - D P L P N P S L T - - - - -
160	K C H P W T S C E T K D L V V Q Q A G T N K T D V V C - - - - -	- - - - - E C - - D P L P N P S L T - - - - -
133	- C R P W T N C S L D G K S V L V N G T K E R D V V C G P S P - - - - -	- - - - - E C - - D P L P N P S L T - - - - -
140	A C K P W T N C T L A G K H T L Q P A S N S S D A I C - - E D - - - - -	- - - - - E C - - D P L P N P S L T - - - - -
167	K C E P V P W N N T F N Y I D V E I T L Y P V N D T S C T R T T - - - - -	- - - - - E C - - D P L P N P S L T - - - - -
167	K C E P V P S N T F N Y I D V E I N L Y P V N D T S C T R T T - - - - -	- - - - - E C - - D P L P N P S L T - - - - -
140	N C T S - - W - - - - -	- - - - - D D I Q C V E E - - - - -

FIG. 2F

		Consensus #1	
198	- - - - -	Q I E N V K G T E D S G T T V I L P L V I F F G - L - - - - -	TNFR1
212	G A V H I L P Q P V S T R S Q H T Q P P T P E P S T A P S T	S F L L P M G P S P P A	TNFR2
200	T P P E G S D S T A P S T Q E P E A P P E Q D L I A S T	- - - V A G V V T T V	NGFR
224	L A I L L S	- - - - -	LTTR
159	- - - - -	- - - - -	- - - - -
130	- A R S S Q A L S P H P Q P T H L P Y V S E M L E A R	- - - G W L - - -	FAS
204	A A S K E L T R A P D S P S S D P G L S P T Q P	- - - T A G H M Q T L	CD27
194	A L V V I P	- - - C P E G S G D C R	CD30
164	D L S P G A S S V T P P A R E P G H S P Q I S	- - - - -	CD40
169	- - - R D P P A T Q P Q E T Q G P P	- - - - -	4-1BB
200	- G L S E S I L T	- - - - -	OX40
200	- G L S E S I L T	- - - - -	VC22
153	- - - - -	- - - F G - - -	TNFR-like

FIG. 2G

FIG. 2H

FIG. 21

FIG. 2J

FIG. 2K

FIG. 21

		Consensus #1	
365	N V P P L R W K E F V R R L G L S D H E I D R L E L Q N G R C L R E A Q Y S M L	TNFR1	
372	P G G H G T Q V N V T C I V N V C S S S D H - S S Q C S S Q A S S T M G D T - -	TNFR2	
355	A G D T W R H L A G E L G Y Q P E H I D S F T H E A C P V R - - - - -	- A L L	
327	P G E H G Q V A H G A N G I H V T G G S V T V T G N I Y I Y N G P V L G G T - -	NGFR	
246	- - - - - K G F V R K N G V N E A K I D E I K N D N V Q D T A E Q K V Q L L	LTTR	
214	- - - R R K Y R S N K G E S P V E P A E P C R Y S C P R - - - - -	FAS	
441	R R S S T Q L R S G A S V T E P V A E E R G L M S Q P L M E T C H S V G A A Y L	CD27	
256	- - - - - H G C Q P V T - - - - -	CD30	
222	- - - - - - - - - - -	CD40	
245	- - - R L P P D - A H K P P G G S F - - - - -	4-1BB	
308	A Q D Y E T D T I S Y R V G N V L D D S H M P G S C N I H K - - - - -	OX40	
311	T Q D Y E T D T I S Y H V G N V L D V D S H M P G R C D T H K - - - - -	VC22	
238	- - - - - - - - - - -	CRMB	

FIG. 2M

pl. No. To be assigned; Group Art Unit: To be assigned
 kt. No. 1488.1280006/EKS/EJH;
 vention: Wei *et al.* ; Tel: 202/371-2600
 itle: Tumor Necrosis Factor Receptor 5

		Consensus #1
405	A T W R R T P R R E A T L E L L G R V I R D M D L L G C	- - - - -
409	- - - D S S P S E S - P K D E - - - Q V P F S K E E C A F	- - - - -
388	A S W A T Q D S A T L D A - - - - -	- - - - -
365	- - - - - R G P G D P - P A P P - - - E P P Y P T P E E G A	- - - - -
279	R N W H Q L H G K K E A - Y D T L I K D L K K A N L - - C T L A E K I Q	- - - - -
239	- - E E E G S T I - - - - -	- - - - -
481	E S L P L Q D A S P A G G - P S S P R D L P E P R V S T E H T N N K I E K I Y I	CD27
263	- - - - - - - - - - -	CD30
222	- - - - - - - - - - -	CD40
260	- - - - - - - - - - -	4-1BB
339	- - - - - - - - - - -	OX40
342	- - - - - - - - - - -	VC22
238	- - - - - - - - - - -	CRMB
		TNFR-like

FIG. 2N

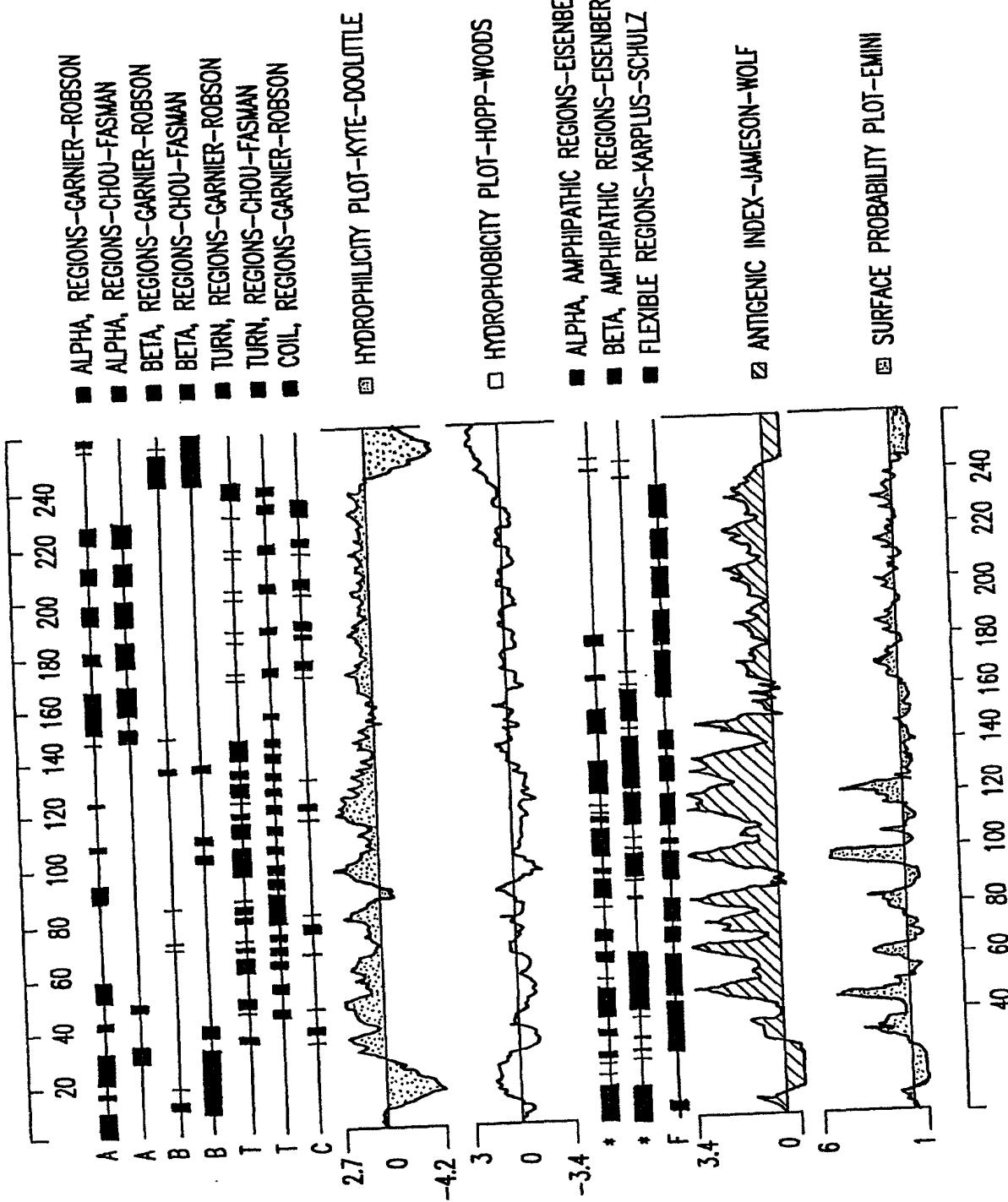
		Consensus #1
434	- - - - - E D I E E A L C G P A A L P - - - - -	- - - - -
431	- - - - -	R S Q L E T P E T L L G S T E K
401	- - - - -	- L I A A L R R I Q R A D
386	- - - - -	T N F R 1
312	- - - T I I L K D I T S D - S E N S N F R - - - - -	T N F R 2
246	- - - - -	N G F R
520	M K A D T V I V G T V K A E L P E G R G L A G P A E P E L E E E L E A D H T P H	E A S
263	- - - - -	CD27
224	F K - - - - -	CD30
260	- - - - -	CD40
345	- - - - -	Q E D G K E S
351	- - - L I V L L I V - - - - -	CD40
251	- - - - -	4-1BB
		R T P OX40
		VC22
		CRM5
		TNFR-like

FIG. 20

Appl. No. To be assigned; Group Art Unit: To be assigned
 Dkt. No. 1488.1280006/EKS/EJH;
 Inventors: Wei *et al.*; Tel: 202/371-2600
 Title: Tumor Necrosis Factor Receptor 5

		Consensus #1	TNFR1	TNFR2	NGFR	LTFR	FAS	CD27	CD30	CD40	4-1BB	OX40	VC22	CRMB	TNFR-like
449	-	· · · · ·	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
448	P	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
413	L	V	E	S	L	C	S	E	S	-	-	-	-	-	-
403	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-
329	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
247	I	Q	E	D	-	Y	R	K	P	-	-	-	-	-	-
560	Y	P	E	Q	E	P	P	L	G	S	C	S	D	V	M
270	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-
236	Q	E	E	D	G	C	-	-	S	C	-	-	-	-	-
263	I	Q	E	E	Q	A	D	A	H	-	-	-	-	-	-
349	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
355	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
258	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

FIG.2P



HPRCB54R

1 GAATTGGCA NAGCCTCTCC ACGCGCACGA ACTCAGCCAA CGATTTCTGA
 51 TAGATTTTG GGAGTTGAC CAGAGATGCA AGGGGTGAAG GAGCGCTTCC
 101 TACCGTTAGG AACTCTGGGG ACAGNNCGCC CCGGCCGCCT GATGGCCGAG
 151 GCAGGGTGCG ACCCAGGACC CAGGACGGCG TCAGGAACCA TACCATGGCC
 201 CGGATCCCCA AGACCTAAA GTTCGTGGTC GTCATCGTCG CGGTCTGCT
 251 GCCAGTCCTA GCTTACTCTG CCACCACTGC CCGGCAGAGG AAGTTNCCA
 301 GCAGNCANTG GNCCCACAGC AACAGNGCA CAGTTCAAG GGGGNAGGAG
 351 TTTTCCANCA AGTTTTATA GTTCAGAACN TATTGGNGCT NTNAACCCTT
 401 GCACAAGGGT TTGGNTTAAA CCAANGTTTC CAANATGNAC TTTTTNGTTC
 451 CCTGTTANAT TTTTTAATTG TTNAAAANTT AAATTNTNA ACCTTNCCNG
 501 GGNAATT

HSJAU57RA

1 GGCAGAGGTG TCTCCAGCCT GGCTCTATCT TCCTCCTTGT NATCGTCCCA
 51 TCCCCACATC CCGTGCACCC CCCAGGACCC TGGTCTCATC AGTCCCTCTC
 101 CTGGAGCTGG GGGTCCACAC ATCTCCCAGC CAAGTCCAAG AGGGCAGGGC
 151 CAGTTCCCTCC CATCTTCAGG CCCAGCCAGG CAGGGGGCAG TCGGCTCCTC
 201 AACTGGGTGA CAAGGGTGAG GATGAGAAGT GGTCACGGGG ATTTATTCAG
 251 CCTTGGTCAG AGCAGAACAC AGAGTTTTC CGTGTGTTGG TTTTACTCT
 301 NNTTCCCCTT CTTNATNCCC CTTTCN

HUSCB54R

1 CCAGGGTCTC CTNCCCCACC TGCTGAAGAG ACANTGACCA CCAGCCCCGGG
 51 GACTCCTGCC TCTTCCTCAT TACCTCTNAT GNANCATCGT AGGGATCATA
 101 GTTCTAATTG TGCTTCTGA ATTGTGCTTT GTTTGGAAAG ACTTCACTGT
 151 GGGAAAGAAAT TCCTTCCTTA CCTGAAGTTG CAGGTAGGCC CTGGGTNAGG
 201 GCGNGGGCG CTGGACANTN TCTGGNCCTG GCTGCCCGCT G

HELBP70R

1 GGCAGAGGCC CCAGCTGCTG AAGAGACAAT AATCACCAGC CCGGGGACTC
 51 CTGNNNTCTNC TNATTACCTC TNATGCACCA TCGTAGGGAT CATACTTCTA
 101 ATTGTGCCTT CTAATTGTTT TTGTTGAAA AGANTTCACT GTGGAAGAAA
 151 TTCTTCCTT ACCTGTAAGT TNCAGGTAGG NGCCTGGCTG AGGGCGGGGG
 201 GCGCTGGTAC ACTCTCTGAC CCTGCCTCCC TCTGNCTGTT TTCCACAGA
 251 CAGAAACGCC TGCCCTGNC CCCAAGTTCC TNGTGTGTTTC CAGCCTGGCT
 301 CTATCTNNC TCCTTGAA TCGTTCCCAT CCCCCACANGC

FIG.4

09866242-040504

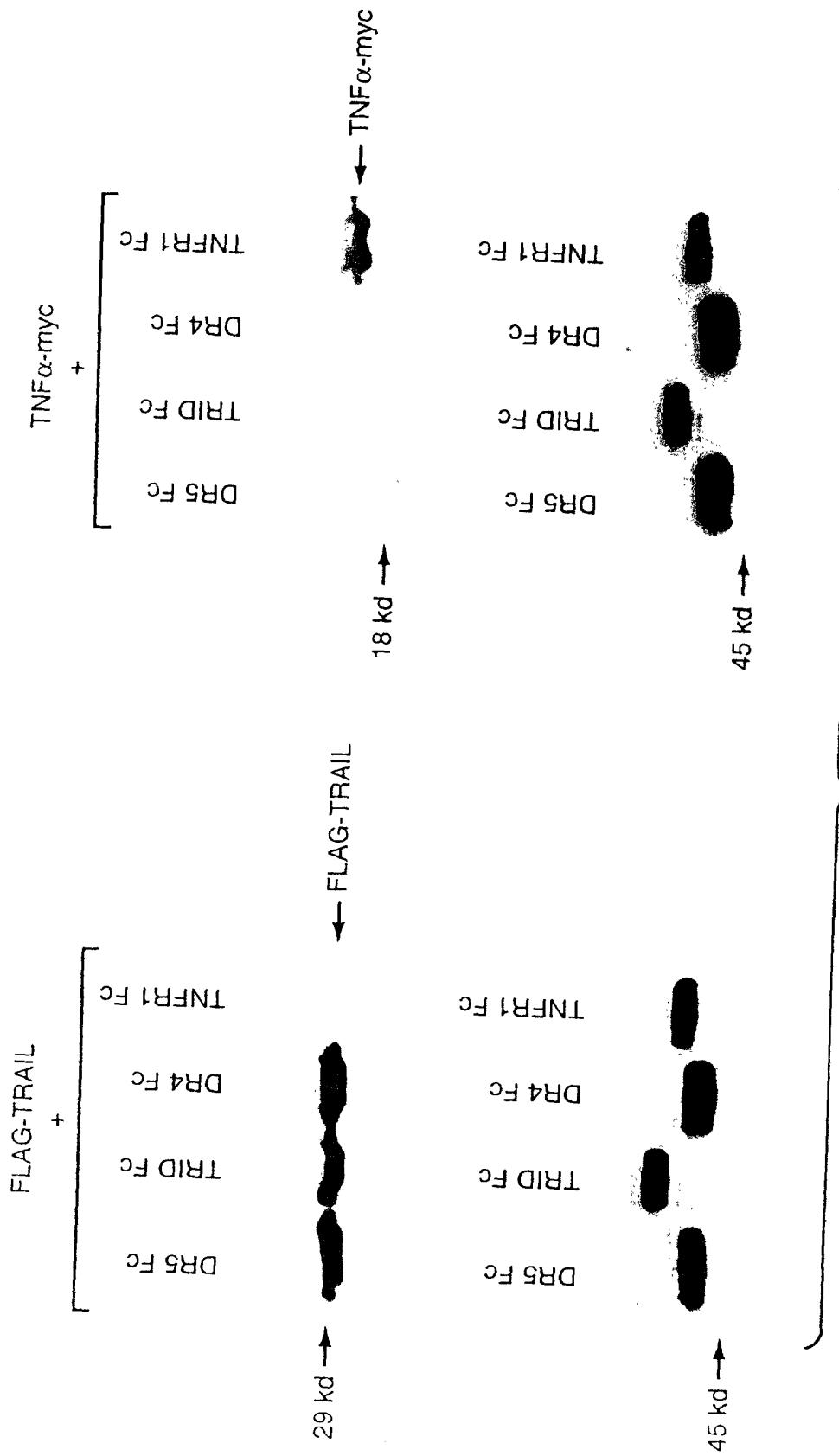


FIG. 5A

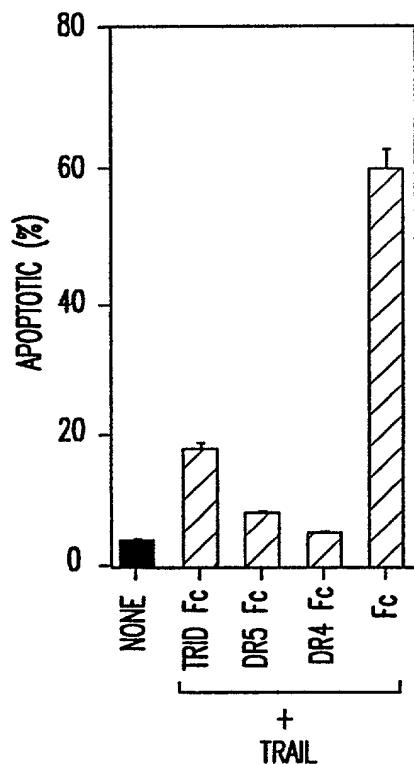


FIG.5B

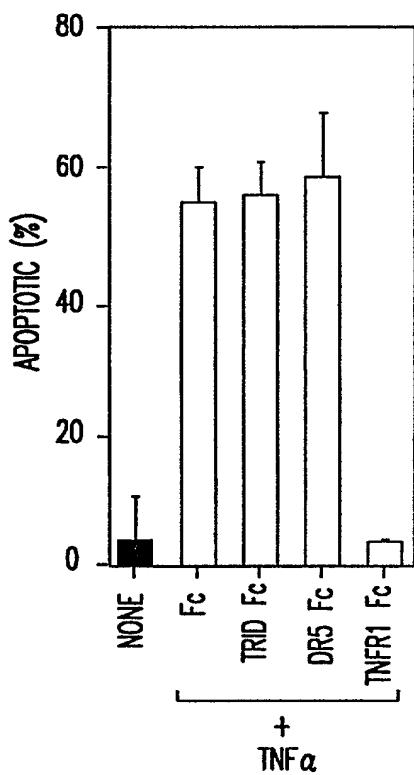


FIG.5C

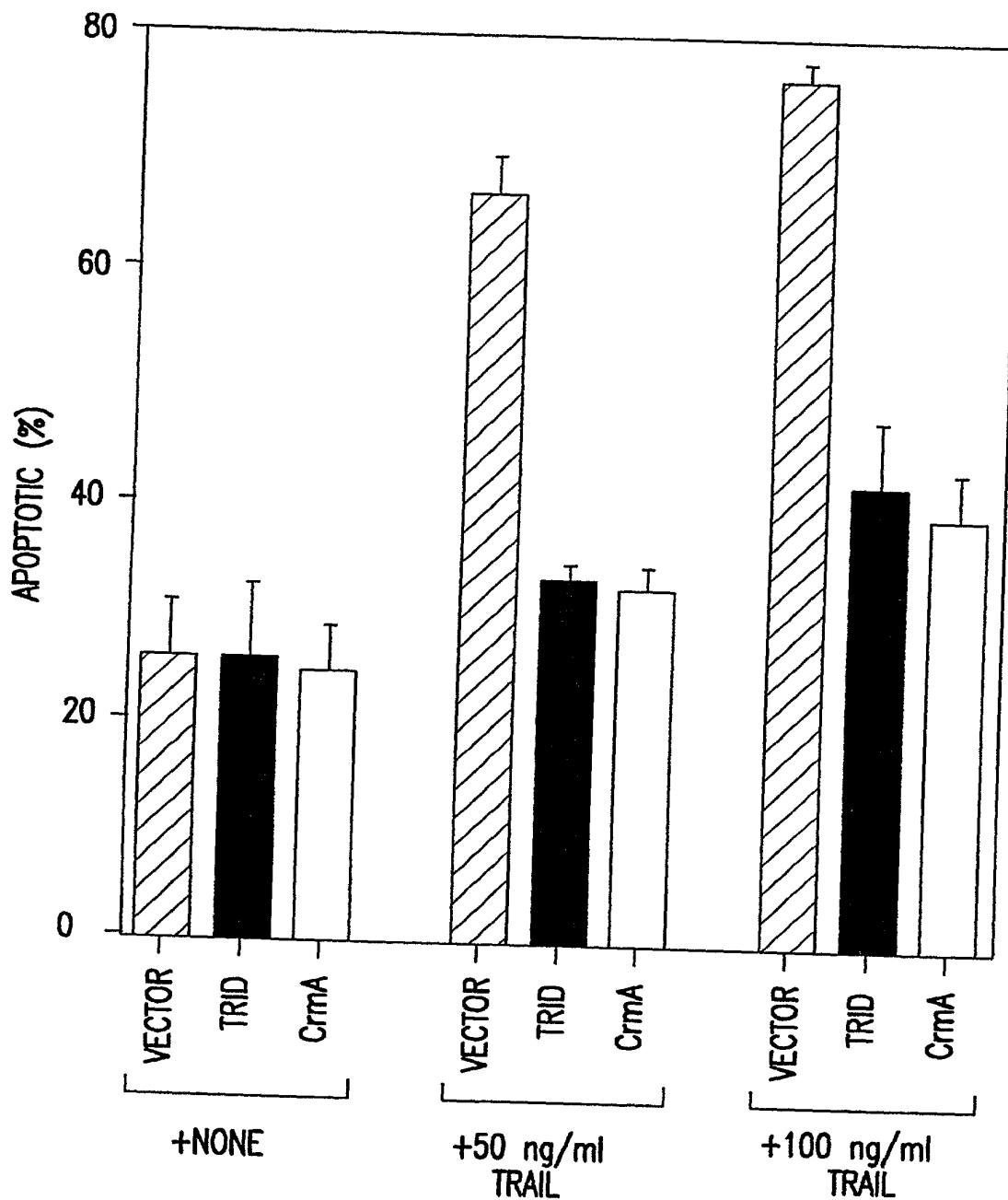


FIG.6